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P.6

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3  <110> APPLICANT: Skeiky, Yasir
4          Reed, Steven
5          Houghton, Raymond L.
6          McNeill, Patricia D.
7          Dillon, Davin C.
8          Lodes, Michael L.
9          Corixa Corporation
11 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
13 <130> FILE REFERENCE: 014058-009041US
15 <140> CURRENT APPLICATION NUMBER: US 09/688,672A
16 <141> CURRENT FILING DATE: 2000-10-10
18 <150> PRIOR APPLICATION NUMBER: US 60/158,338
19 <151> PRIOR FILING DATE: 1999-10-07
21 <150> PRIOR APPLICATION NUMBER: US 60/158,425
22 <151> PRIOR FILING DATE: 1999-10-07
24 <160> NUMBER OF SEQ ID NOS: 202
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 2220
30 <212> TYPE: DNA
31 <213> ORGANISM: Mycobacterium tuberculosis
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35 <222> LOCATION: (1)..(2220)
36 <223> OTHER INFORMATION: Mtb81
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41  1               5                   10                  15
43 gac ttc gtg aac aat gaa gcc ctg cct ggc acc gat atc gac ccg gac    96
44 Asp Phe Val Asn Asn Glu Ala Leu Pro Gly Thr Asp Ile Asp Pro Asp
45                  20                  25                  30
47 agc ttc tgg gcg ggc gtc gac aar gtc gtc gcc gac ctg acc ccg cag   144
48 Ser Phe Trp Ala Gly Val Asp Lys Val Val Ala Asp Leu Thr Pro Gln
49          35                  40                  45
51 aac caa gct ctg ttg aac gcc cgc gac gag ctg cag gcg cag atc gac   192
52 Asn Gln Ala Leu Leu Asn Ala Arg Asp Glu Leu Gln Ala Gln Ile Asp
53      50                  55                  60
55 aag tgg cac cgg cgt cgg gtg atc gag ccc atc gac atg gat gcc tac   240
56 Lys Trp His Arg Arg Arg Val Ile Glu Pro Ile Asp Met Asp Ala Tyr
57  65                  70                  75                  80
59 cgc cag ttc ctc acc gag atc ggc tac ctg ctt ccc gaa cct gat gac   288
60 Arg Gln Phe Leu Thr Glu Ile Gly Tyr Leu Leu Pro Glu Pro Asp Asp
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2/1

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63  ttc acc atc acc acg tcc ggt gtc gac gct gag atc acc acg acc gcc    336
64  Phe Thr Ile Thr Thr Ser Gly Val Asp Ala Glu Ile Thr Thr Thr Ala
65             100                   105                   110
67  ggc ccc cag ctg gtg gtg ccg gtg ctc aac gcg cgg ttt gct ctg aac    384
68  Gly Pro Gln Leu Val Val Pro Val Leu Asn Ala Arg Phe Ala Leu Asn
69             115                   120                   125
71  gcg gcc aac gct cgc tgg ggc tcc ctc tac gac gcc ttg tat ggc acc    432
72  Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr
73             130                   135                   140
75  gat gtc atc ccc gag acc gac ggc gcc gaa aaa ggc ccc acg tac aac    480
76  Asp Val Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Pro Thr Tyr Asn
77  145                   150                   155                   160
79  aag gtt cgt ggc gac aag gtg atc gcg tat gcc cgc aag ttc ctc gac    528
80  Lys Val Arg Gly Asp Lys Val Ile Ala Tyr Ala Arg Lys Phe Leu Asp
81             165                   170                   175
83  gac agt gtt ccg ctg tcg tcg ggt tcc ttt ggc gac gcc acc ggt ttc    576
84  Asp Ser Val Pro Leu Ser Ser Gly Ser Phe Gly Asp Ala Thr Gly Phe
85             180                   185                   190
87  aca gtg cag gat ggc cag ctc gtg gtt gcc ttg ccg gat aag tcc acc    624
88  Thr Val Gln Asp Gly Gln Leu Val Val Ala Leu Pro Asp Lys Ser Thr
89             195                   200                   205
91  ggc ctg gcc aac ccc ggc cag ttc gcc ggc tac acc ggc gca gcc gag    672
92  Gly Leu Ala Asn Pro Gly Gln Phe Ala Gly Tyr Thr Gly Ala Ala Glu
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95  tcg ccg aca tcg gtg ctg cta atc aat cac ggt ttg cac atc gag atc    720
96  Ser Pro Thr Ser Val Leu Leu Ile Asn His Gly Leu His Ile Glu Ile
97  225                   230                   235                   240
99  ctg atc gat ccg gag tcg cag gtc ggc acc acc gac cgg gcc ggc gtc    768
100 Leu Ile Asp Pro Glu Ser Gln Val Gly Thr Thr Asp Arg Ala Gly Val
101                   245                   250                   255
103 aag gac gtg atc ctg gaa tcc gcg atc acc acg atc atg gac ttc gag    816
104 Lys Asp Val Ile Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu
105                   260                   265                   270
107 gac tcg gtg gcc gcc gtg gac gcc gcc gac aag gtg ctg ggt tat cgg    864
108 Asp Ser Val Ala Ala Val Asp Ala Ala Asp Lys Val Leu Gly Tyr Arg
109                   275                   280                   285
111 aac tgg ctc ggc ctg aac aag ggc gac ctg gca gca gcg gta gac aag    912
112 Asn Trp Leu Gly Leu Asn Lys Gly Asp Leu Ala Ala Ala Val Asp Lys
113                   290                   295                   300
115 gac ggc acc gct ttc ctg cgg gtg ctc aat agg gac cgg aac tac acc    960
116 Asp Gly Thr Ala Phe Leu Arg Val Leu Asn Arg Asp Arg Asn Tyr Thr
117 305                   310                   315                   320
119 gca ccc ggc ggt ggc cag ttc acg ctg cct gga cgc agc ctc atg ttc   1008
120 Ala Pro Gly Gly Gly Gln Phe Thr Leu Pro Gly Arg Ser Leu Met Phe
121                   325                   330                   335
123 gtc cgc aac gtc ggt cac ttg atg acg aat gac gcc atc gtc gac act   1056
124 Val Arg Asn Val Gly His Leu Met Thr Asn Asp Ala Ile Val Asp Thr
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127 gac ggc agc gag gtg ttc gaa ggc atc atg gat gcc cta ttc acc ggc   1104
128 Asp Gly Ser Glu Val Phe Glu Gly Ile Met Asp Ala Leu Phe Thr Gly
129         355             360                 365
131 ctg atc gcc atc cac ggg cta aag gcc agc gac gtc aac ggg ccg ctg   1152
132 Leu Ile Ala Ile His Gly Leu Lys Ala Ser Asp Val Asn Gly Pro Leu
133     370             375                 380
135 atc aac agc cgc acc ggc tcc atc tac atc gtc aag ccg aag atg cac   1200
136 Ile Asn Ser Arg Thr Gly Ser Ile Tyr Ile Val Lys Pro Lys Met His
137 385             390                 395                 400
139 ggt ccg gcc gag gtg gcg ttt acc tgc gaa ctg ttc agc cgg gtt gaa   1248
140 Gly Pro Ala Glu Val Ala Phe Thr Cys Glu Leu Phe Ser Arg Val Glu
141             405             410                 415
143 gat gtg ctg ggg ttg ccg caa aac acc atg aag atc ggc atc atg gac   1296
144 Asp Val Leu Gly Leu Pro Gln Asn Thr Met Lys Ile Gly Ile Met Asp
145             420             425                 430
147 gag gaa cgc cgg acc acg gtc aac ctc aag gcg tgc atc aaa gct gcc   1344
148 Glu Glu Arg Arg Thr Thr Val Asn Leu Lys Ala Cys Ile Lys Ala Ala
149         435             440                 445
151 gcg gac cgc gtg gtg ttc atc aac acc ggg ttc ctg gac cgc acc ggc   1392
152 Ala Asp Arg Val Val Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly
153     450             455                 460
155 gat gaa atc cac acc tcg atg gag gcc ggc ccg atg gtg cgc aag ggc   1440
156 Asp Glu Ile His Thr Ser Met Glu Ala Gly Pro Met Val Arg Lys Gly
157 465             470                 475                 480
159 acc atg aag agc cag ccg tgg atc ttg gcc tac gag gac cac aac gtc   1488
160 Thr Met Lys Ser Gln Pro Trp Ile Leu Ala Tyr Glu Asp His Asn Val
161             485             490                 495
163 gat gcc ggc ctg gcc gcc ggg ttc agc ggc cga gcc cag gtc ggc aag   1536
164 Asp Ala Gly Leu Ala Ala Gly Phe Ser Gly Arg Ala Gln Val Gly Lys
165         500             505                 510
167 ggc atg tgg aca atg acc gag ctg atg gcc gac atg gtc gag aca aaa   1584
168 Gly Met Trp Thr Met Thr Glu Leu Met Ala Asp Met Val Glu Thr Lys
169     515             520                 525
171 atc gcc cag ccg cgc gcc ggg gcc agc acc gcc tgg gtt ccc tct ccc   1632
172 Ile Ala Gln Pro Arg Ala Gly Ala Ser Thr Ala Trp Val Pro Ser Pro
173     530             535                 540
175 act gcg gcc acc ctg cat gcg ctg cac tac cac cag gtc gac gtc gcc   1680
176 Thr Ala Ala Thr Leu His Ala Leu His Tyr His Gln Val Asp Val Ala
177 545             550                 555                 560
179 gcg gtg caa caa gga ctg gcg ggg aag cgt cgc gcc acc atc gaa caa   1728
180 Ala Val Gln Gln Gly Leu Ala Gly Lys Arg Arg Ala Thr Ile Glu Gln
181             565             570                 575
183 ttg ctg acc att ccg ctg gcc aag gaa ttg gcc tgg gct ccc gac gag   1776
184 Leu Leu Thr Ile Pro Leu Ala Lys Glu Leu Ala Trp Ala Pro Asp Glu
185             580             585                 590
187 atc cgc gaa gag gtc gac aac aac tgt caa tcc atc ctc ggc tac gtg   1824
188 Ile Arg Glu Glu Val Asp Asn Asn Cys Gln Ser Ile Leu Gly Tyr Val
189         595             600                 605
191 gtt cgc tgg gtt gat caa ggt gtc ggc tgc tcg aag gtg ccc gac atc   1872
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/688,672A

DATE: 02/11/2003
TIME: 10:51:54

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Output Set: N:\CRF4\02112003\I688672A.raw

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195 cac gac gtc gcg ctc atg gag gac cgg gcc acg ctg cga atc tcc agc      1920
196 His Asp Val Ala Leu Met Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser
197 625                 630             635                 640
199 caa ttg ttg gcc aac tgg ctg cgc cac ggt gtg atc acc agc gcg gat      1968
200 Gln Leu Leu Ala Asn Trp Leu Arg His Gly Val Ile Thr Ser Ala Asp
201             645             650                 655
203 gtg cgg gcc agc ttg gag cgg atg gcg ccg ttg gtc gat cga caa aac      2016
204 Val Arg Ala Ser Leu Glu Arg Met Ala Pro Leu Val Asp Arg Gln Asn
205         660             665                 670
207 gcg ggc gac gtg gca tac cga ccg atg gca ccc aac ttc gac gac agt      2064
208 Ala Gly Asp Val Ala Tyr Arg Pro Met Ala Pro Asn Phe Asp Asp Ser
209             675             680             685
211 atc gcc ttc ctg gcc gcg cag gag ctg atc ttg tcc ggg gcc cag cag      2112
212 Ile Ala Phe Leu Ala Ala Gln Glu Leu Ile Leu Ser Gly Ala Gln Gln
213     690                 695             700
215 ccc aac ggc tac acc gag ccg atc ctg cac cga cgt cgt cgg gag ttt      2160
216 Pro Asn Gly Tyr Thr Glu Pro Ile Leu His Arg Arg Arg Arg Glu Phe
217 705                 710             715                 720
219 aag gcc cgg gcc gct gag aag ccg gcc cca tcg gac agg gcc ggt gac      2208
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221             725             730                 735
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224 Asp Ala Ala Arg                                                      2220
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238             20                  25              30
240 Ser Phe Trp Ala Gly Val Asp Lys Val Val Ala Asp Leu Thr Pro Gln
241         35                  40              45
243 Asn Gln Ala Leu Leu Asn Ala Arg Asp Glu Leu Gln Ala Gln Ile Asp
244         50                  55              60
246 Lys Trp His Arg Arg Arg Val Ile Glu Pro Ile Asp Met Asp Ala Tyr
247 65                  70              75                  80
249 Arg Gln Phe Leu Thr Glu Ile Gly Tyr Leu Leu Pro Glu Pro Asp Asp
250             85                  90                  95
252 Phe Thr Ile Thr Thr Ser Gly Val Asp Ala Glu Ile Thr Thr Thr Ala
253             100                 105             110
255 Gly Pro Gln Leu Val Val Pro Val Leu Asn Ala Arg Phe Ala Leu Asn
256         115                 120             125
258 Ala Ala Asn Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr
259     130                 135             140
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261 Asp Val Ile Pro Glu Thr Asp Gly Ala Glu Lys Gly Pro Thr Tyr Asn
262 145                 150                 155                 160
264 Lys Val Arg Gly Asp Lys Val Ile Ala Tyr Ala Arg Lys Phe Leu Asp
265                 165                 170                 175
267 Asp Ser Val Pro Leu Ser Ser Gly Ser Phe Gly Asp Ala Thr Gly Phe
268                 180                 185                 190
270 Thr Val Gln Asp Gly Gln Leu Val Val Ala Leu Pro Asp Lys Ser Thr
271             195                 200                 205
273 Gly Leu Ala Asn Pro Gly Gln Phe Ala Gly Tyr Thr Gly Ala Ala Glu
274         210                 215                 220
276 Ser Pro Thr Ser Val Leu Leu Ile Asn His Gly Leu His Ile Glu Ile
277 225                 230                 235                 240
279 Leu Ile Asp Pro Glu Ser Gln Val Gly Thr Thr Asp Arg Ala Gly Val
280                 245                 250                 255
282 Lys Asp Val Ile Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu
283                 260                 265                 270
285 Asp Ser Val Ala Ala Val Asp Ala Ala Asp Lys Val Leu Gly Tyr Arg
286         275                 280                 285
288 Asn Trp Leu Gly Leu Asn Lys Gly Asp Leu Ala Ala Ala Val Asp Lys
289     290                 295                 300
291 Asp Gly Thr Ala Phe Leu Arg Val Leu Asn Arg Asp Arg Asn Tyr Thr
292 305                 310                 315                 320
294 Ala Pro Gly Gly Gly Gln Phe Thr Leu Pro Gly Arg Ser Leu Met Phe
295                 325                 330                 335
297 Val Arg Asn Val Gly His Leu Met Thr Asn Asp Ala Ile Val Asp Thr
298             340                 345                 350
300 Asp Gly Ser Glu Val Phe Glu Gly Ile Met Asp Ala Leu Phe Thr Gly
301         355                 360                 365
303 Leu Ile Ala Ile His Gly Leu Lys Ala Ser Asp Val Asn Gly Pro Leu
304     370                 375                 380
306 Ile Asn Ser Arg Thr Gly Ser Ile Tyr Ile Val Lys Pro Lys Met His
307 385                 390                 395                 400
309 Gly Pro Ala Glu Val Ala Phe Thr Cys Glu Leu Phe Ser Arg Val Glu
310                 405                 410                 415
312 Asp Val Leu Gly Leu Pro Gln Asn Thr Met Lys Ile Gly Ile Met Asp
313         420                 425                 430
315 Glu Glu Arg Arg Thr Thr Val Asn Leu Lys Ala Cys Ile Lys Ala Ala
316     435                 440                 445
318 Ala Asp Arg Val Val Phe Ile Asn Thr Gly Phe Leu Asp Arg Thr Gly
319     450                 455                 460
321 Asp Glu Ile His Thr Ser Met Glu Ala Gly Pro Met Val Arg Lys Gly
322 465                 470                 475                 480
324 Thr Met Lys Ser Gln Pro Trp Ile Leu Ala Tyr Glu Asp His Asn Val
325             485                 490                 495
327 Asp Ala Gly Leu Ala Ala Gly Phe Ser Gly Arg Ala Gln Val Gly Lys
328         500                 505                 510
330 Gly Met Trp Thr Met Thr Glu Leu Met Ala Asp Met Val Glu Thr Lys
331         515                 520                 525
333 Ile Ala Gln Pro Arg Ala Gly Ala Ser Thr Ala Trp Val Pro Ser Pro
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 02/11/2003
PATENT APPLICATION: US/09/688,672A   TIME: 10:51:55

Input Set : A:\-90-4-1.app
Output Set: N:\CRF4\02112003\I688672A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:11; N Pos. 325,328,348,353,442,659,679
Seq#:12; Xaa Pos. 63,121,285
Seq#:29; N Pos. 1460,1854
Seq#:33; N Pos. 497,500,1136,1445,1487,1509,1515
Seq#:155; N Pos. 104